SEQUENCE LISTING

```
<110> Sacktor, Todd C.
<120> A MEMORY ENHANCING PROTEIN
<130> The Research Foundation Albany
<140> 09/839.073
<141> 2001-04-20
<160> 4
<170> PatentIn Ver. 2.1
<210> 1
<211> 2058
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (444)..(1670)
<220>
<221> unsure
<222> (522)
<223> r at position 522 is g or a
<400> 1
cccgggcctg gagacatgag gaggcaggga tgtgaggggc gggggacagg acagccggcc 60
ttccgttaaa tatctgctcc tcgcgctcga gcctccctgc ctattgtcgg ggccggagcg 120
aagccgacgc agcatcagct cgtcaacggg aaggaagatg cctccctgca cgcccgccgc 180
gcacagagca taaagaatct gcgctgagga ggcaggagaa gaaagccgaa tctatctacc 240
gccggggagc cagaagatgg aggaagctgt accgtgccaa cggccacctc ttccaagcca 300
agcgctttaa caggagagcg tactgcggtc agtgcagcga gaggatatgg ggcctcgcga 360
ggcaaggcta caggtgcatc aactgcaaac tgctggtcca taagcgctgc cacggcctcg 420
tecegetgae etgeaggaag eat atg gat tet gte atg eet tee eaa gag eet 473
                             Met Asp Ser Val Met Pro Ser Gln Glu Pro
cca gta gac gac aag aac gag gac gcc gac ctt cct tcc gag gag aca
Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr
15 20 25
                                                                          521
rat gga att gct tac att tcc tca tcc cgg aag cat gac agc att aaa
Xaa Gly Ile Ala Tyr Ile Ser Ser Arg Lys His Asp Ser Ile Lys
gac gac tcg gag gac ctt aag cca gtt atc gat ggg atg gat gga atc
Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile
45 50 55
                                                                          617
                                                                          665
aaa atc tct cag ggg ctt ggg ctg cag gac ttt gac cta atc aga gtc
Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val
```

atc ggg cgc ggg agc tac gcc aag gtt ctc ctg gtg cgg ttg aag aag Ile Gly Arg Gly Ser Tyr Ala Lys Val Leu Leu Val Arg Leu Lys Lys 75 80 85 90 713 aat gac caa att tac gcc atg aaa gtg gtg aag aaa gag ctg gtg cat Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val His 95 100 105 761 gat gac gag gat att gac tgg gta cag aca gag aag cac gtg ttt gag Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe Glu 809 cag gca tcc agc aac ccc ttc ctg gtc gga tta cac tcc tgc ttc cag Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe Gln 857 acg aca agt cgg ttg ttc ctg gtc att gag tac gtc aac ggc ggg gac Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly Asp 905 140 ctg atg ttc cac atg cag agg cag agg aag ctc cct gag gag cac gcc 953 Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His Ala agg ttc tac gcg gcc gag atc tgc atc gcc ctc aac ttc ctg cac gag 1001 Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His Glu agg ggg atc atc tac agg gac ctg aag ctg gac aac gtc ctc ctg gat Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp 190 195 200 1049 gcg gac ggg cac atc aag ctc aca gac tac ggc atg tgc aag gaa ggc Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly 205 210 1097 ggc cct ggt gac aca acg agc act ttc tgc gga acc ccg aat tac Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr 220 225 230 1145 atc gcc ccc gaa atc ctg cgg gga gag gag tac ggg ttc agc gtg gac Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp 235 240 245 250 1193 tgg tgg gcg ctg gga gtc ctc atg ttt gag atg atg gcc ggg cgc tcc Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg Ser 255 260 265 1241 1289 ccg ttc gac atc atc acc gac aac ccg gac atg aac aca gag gac tac Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr ctt ttc caa gtg atc ctg gag aag ccc atc cgg atc ccc cgg ttc ctg Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu 285 290 295 1337 tcc gtc aaa gcc tcc cat gtt tta aaa gga ttt tta aat aag gac ccc Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp Pro 1385 300 305 aaa gag agg ctc ggc tgc cgg cca cag act gga ttt tct gac atc aag Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys 315 320 325 330 1433

1481 tcc cac gcg ttc ttc cgc agc ata gac tgg gac ttg ctg gag aag aag Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys 340 cag gcg ctc cct cca ttc cag cca cag atc aca gac gac tac ggt ctg Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu 1529 1577 gac aac ttt gac aca cag ttc acc agc gag ccc gtg cag ctg acc cca Asp Asn Phe Asp Thr Glñ Phe Thr Ser Glũ Pro Val Glñ Leu Thr Pro gac gat gag gat gcc ata aag agg atc gac cag tca gag ttc gaa ggc 1625 ÁSP ÁSP Ğlü ÁSP Ála Ile Lys Arg Ile ÁSP Gln Ser Glu Phe Glu Gly 380 385 ttt gag tat atc aac cca tta ttg ctg tcc acc gag gag tcg gtg Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val 1670 395 400 405 tgaggccgcg tgcgtctctg tcgtggacac gcgtgattga ccctttaact gtatccttaa 1730 ccaccgcata tgcatgccag gctgggcacg gctccgaggg cggccaggga cagacgcttg 1790 cgccgagacc gcagagggaa gcgtcagcgg gcgctgctgg gagcagaaca gtccctcaca 1850 cctqqcccqq caqqcaqctt cqtqctqqaq qaacttqctq ctqtqcctgc gtcgcggcgg 1910 atccgcgggg accctgccga gggggctgtc atgcggtttc caaggtgcac attttccacg 1970 gaaacagaac tcgatgcact gacctgctcc gccaggaaag tgagcgtgta gcgtcctgag 2030 2058 gaataaaatg ttccgatgaa aaaaaaaa

```
<210> 2
<211> 409
<212> PRT
<213> Homo sapiens
<220>
<221> unsure
<222> (27)
<223> Xaa at position 27 is Asp or Asn
```

Met Lys Val Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp 100 105 110 Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro 115 120 125 Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe 130 140 Leu Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln 145 150 155 160 Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu 165 170 175 Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg 180 185 190 Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys 195 200 205 Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr 210 215 220 Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu 225 230 235 240 Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val 245 250 255 Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr 260 265 270 Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu 275 280 285 Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His 290 295 300 Val Leu Lys Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys 315 315 320 Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg 325 330 335 Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe 340 345 350 Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln
355 360 365 Phe Thr Ser Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile 370 375 380 Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro 385 390 395 400 Leu Leu Ser Thr Glu Glu Ser Val 405

```
<213> Homo sapiens
<400> 3
999cccggac ctctgtactc ctccgtccct acactccccg cccctgtcc tgtcggccgg 60
aaggcaattt atagacgagg agcgcgagct cggagggacg gataacagcc ccggcctcgc 120
ttcggctgcg tcgtagtcga gcagttgccc ttccttctac ggagggacgt gcgggcggcg 180
cgtgtctcgt atttcttaga cgcgactcct ccgtcctctt ctttcggctt agatagatgg 240
CGGCCCCTCG gtcttctacc tccttcgaca tggcacggtt gccggtggag aaggttcggt 300 tcgcgaaatt gtcctctcgc atgacgccag tcacgtcgct ctcctatacc ccggagggct 360 ccgttccgat gtccacgtag ttgacgtttg acgaccaggt attcgcgacg gtgccggagc 420 agggcgactg gacgtccttc gtatacctaa gacagtacgg aagggttctc ggaggtcatc 480 tgctgttctt gctcctgcgg ctggaaggaa ggctccttg tctaccttaa cgaatgtaaa 540 ggagtagggc cttcgtactg tcgtaaattc tgcgaagca cctggaattc ggtcaatagc 660
taccctacct accttagttť tagagagtcc ccgaacccga cgtcctgaaa ctggattagt 660
ctcagtagec egegeceteg atgeggitee aagaggaeca egecaaette tteitaetgg 720
tttaaatgcg gtactttcac cacttctttc tcgaccacgt actactgctc ctataactga 780
cccatgtctg tctcttcgtg cacaaactcg tccgtaggtc gttggggaag gaccagccta 840
atgtgaggac gaaggtcīgc tgttcagccā acaaggācca ģtaācīcatģ cagttģccgc 900
ccctggacta caaggtgtac gtctccgtct ccttcgaggg actcctcgtg cggtccaaga 960 tgcgccggct ctagacgtag cgggagttga aggacgtgct ctcccctag tagatgtccc 1020 tggacttcga cctgttgcag gaggacctac gcctgccgt gtagttcgag tgtctgatgc 1080 cgtacacgtt ccttccggac ccgggaccac tgtgttgctc gtgaaagacg ccttggggct 1140 taatgtagcg ggggctttag gacgccctc tcctcatgcc caagtcgcac ctgaccaccc 1200
gcgaccctca ggagtacaaa ctctactacc ggcccgcgag gggcaagctg tagtagtggc 1260
tgttgggcct gtacttgtgt ctcctgatgg aaaaggttca ctaggacctc ttcgggtagg 1320
cctagggggc caaggacagg cagtttcgga gggtacaaaa ttttcctaaa aatttattcc 1380
tggggtttct ctccgagccg acggccggtg tctgacctaa aagactgtag ttcagggtgc 1440
gcaagaaggc gtcgtatctg accctgaacg acctcttctt cgtccgcgag ggaggtaagg 1500 tcggtgtcta gtgtctgctg atgccagacc tgttgaaact gtgtgtcaag tggtcgctcg 1560 ggcacgtcga ctggggtctg ctactcctac ggtattctc ctagctggtc agtctcaagc 1620
ttccgaaact catatagttg ggtaataacg acaggtggct cctcagccac actccggcgc 1680
acgcagagac agcacctgtg cgcactaact gggaaattga cataggaatt ggtggcgtat 1740
acgtacggtc cgacccgtgc cgaggctccc gccggtccct gtctgcgaac gcggctctgg 1800
cgtctccctt cgcagtcgcc cgcgacgacc ctcgtcttgt cagggagtgt ggaccgggcc 1860
gtccgtcgaa gcacgacctc cttgaacgac gacacggacg cagcgccgcc taggcgcccc 1920 tgggacggct cccccgacag tacgccaaag gttccacgtg taaaaggtgc ctttgtcttg 1980 agctacgtga ctggacgagg cggtcctttc actcgcacat cgcaggactc cttattttac 2040
aaggctactt ttttttt
                                                                                                       2058
<210> 4
<211> 13
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: mzip peptide
<400> 4
Ser lle Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu
1 10
```

<212> DNA